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RAW SEQUENCE LISTING
PATENT APPLICATION: US/10/002,244A

DATE: 04/18/2002
TIME: 14:12:54

Input Set : A:\346BUSC1.txt
Output Set: N:\CRF3\04182002\J002244A.raw

3 <110> APPLICANT: ARIAD Gene Therapeutics, Inc.
5 <120> TITLE OF INVENTION: Use of Heterologous Transcription Factors in Gene Therapy
7 <130> FILE REFERENCE: 346B USC1
9 <140> CURRENT APPLICATION NUMBER: 10/002,244A
10 <141> CURRENT FILING DATE: 2001-10-23
12 <160> NUMBER OF SEQ ID NOS: 68
14 <170> SOFTWARE: PatentIn version 3.0
16 <210> SEQ ID NO: 1
17 <211> LENGTH: 8
18 <212> TYPE: PRT
19 <213> ORGANISM: herpes simplex virus 7
21 <220> FEATURE:
22 <221> NAME/KEY: DOMAIN
23 <222> LOCATION: (1)..(8)
24 <223> OTHER INFORMATION: VP16 V8 motif
27 <400> SEQUENCE: 1
29 Asp Phe Asp Leu Asp Met Leu Gly
30 1 5
32 <210> SEQ ID NO: 2
33 <211> LENGTH: 9
34 <212> TYPE: PRT
35 <213> ORGANISM: herpes simplex virus 7
37 <220> FEATURE:
38 <221> NAME/KEY: DOMAIN
39 <222> LOCATION: (1)..(9)
40 <223> OTHER INFORMATION: VP16 V9 motif
43 <400> SEQUENCE: 2
45 Asp Phe Asp Leu Asp Met Leu Gly Gly
46 1 5
48 <210> SEQ ID NO: 3
49 <211> LENGTH: 12
50 <212> TYPE: DNA
51 <213> ORGANISM: Artificial Sequence
53 <220> FEATURE:
54 <221> NAME/KEY: misc_feature
55 <222> LOCATION: (1)..(12)
56 <223> OTHER INFORMATION: ZFHD1 composite DNA-binding site
57 n = A, G, T or C
60 <400> SEQUENCE: 3
W--> 61 taattanggg ng 12
64 <210> SEQ ID NO: 4
65 <211> LENGTH: 18
66 <212> TYPE: PRT

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67 <213> ORGANISM: homo sapien
69 <220> FEATURE:
70 <221> NAME/KEY: DOMAIN
71 <222> LOCATION: (1)..(18)
72 <223> OTHER INFORMATION: glutamine rich region of Oct-2
75 <400> SEQUENCE: 4
77 Asn Phe Leu Gln Leu Pro Gln Gln Thr Gln Gly Ala Leu Leu Thr Ser
78 1 5 10 15
80 Gln Pro
83 <210> SEQ ID NO: 5
84 <211> LENGTH: 6
85 <212> TYPE: PRT
86 <213> ORGANISM: homo sapien
88 <220> FEATURE:
89 <221> NAME/KEY: DOMAIN
90 <222> LOCATION: (1)..(6)
91 <223> OTHER INFORMATION: repeat in Ewing sarcome gene
94 <400> SEQUENCE: 5
96 Ser Tyr Gly Gln Gln Ser
97 1 5
99 <210> SEQ ID NO: 6
100 <211> LENGTH: 31
101 <212> TYPE: DNA
102 <213> ORGANISM: Artificial Sequence
104 <220> FEATURE:
105 <221> NAME/KEY: misc_feature
106 <222> LOCATION: (1)..(31)
107 <223> OTHER INFORMATION: primer
110 <400> SEQUENCE: 6
111 atgctctaga gaacgccat atgcttgccc t 31
114 <210> SEQ ID NO: 7
115 <211> LENGTH: 34
116 <212> TYPE: DNA
117 <213> ORGANISM: Artificial Sequence
119 <220> FEATURE:
120 <221> NAME/KEY: misc_feature
121 <222> LOCATION: (1)..(34)
122 <223> OTHER INFORMATION: primer
125 <400> SEQUENCE: 7
126 atgcgcggcc gccgcctgtg tgggtgcgga tgtg 34
129 <210> SEQ ID NO: 8
130 <211> LENGTH: 33
131 <212> TYPE: DNA
132 <213> ORGANISM: Artificial Sequence
134 <220> FEATURE:
135 <221> NAME/KEY: misc_feature
136 <222> LOCATION: (1)..(33)
137 <223> OTHER INFORMATION: primer
140 <400> SEQUENCE: 8

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141 atgcgcggcc gcaggaggaa gaaacgcacc agc
144 <210> SEQ ID NO: 9
145 <211> LENGTH: 49
146 <212> TYPE: DNA
147 <213> ORGANISM: Artificial Sequence
149 <220> FEATURE:
150 <221> NAME/KEY: misc_feature
151 <222> LOCATION: (1)..(49)
152 <223> OTHER INFORMATION: primer
155 <400> SEQUENCE: 9
156 gcatggatcc gattcaacta gtgttattc tttttcttt ctggcggcg 49
159 <210> SEQ ID NO: 10
160 <211> LENGTH: 306
161 <212> TYPE: DNA
162 <213> ORGANISM: homo sapien
164 <220> FEATURE:
165 <221> NAME/KEY: misc_feature
166 <222> LOCATION: (1)..(306)
167 <223> OTHER INFORMATION: 100 aa of p65 transcription activation domain
170 <400> SEQUENCE: 10
171 ctgggggcct tgcttggcaa cagcacagac ccagctgtgt tcacagaccc ggcattccgtc 60
173 gaaactccg agttttagca gctgctgaac cagggcatac ctgtggccccc ccacacaact 120
175 gagcccatgc tgatggatg ccctgaggct ataactcgcc tagtgacagg ggcccagagg 180
177 ccccccggacc cagctcctgc tccactgggg gccccggggc tccccaatgg cctccttca 240
179 ggagatgaag acttcttc cattgcggac atggacttct cagccctgtc gagtcagatc 300
181 agctcc 306
184 <210> SEQ ID NO: 11
185 <211> LENGTH: 573
186 <212> TYPE: DNA
187 <213> ORGANISM: homo sapien
189 <220> FEATURE:
190 <221> NAME/KEY: misc_feature
191 <222> LOCATION: (1)..(573)
193 <400> SEQUENCE: 11
194 gatgagtttc ccaccatggt gttccttct gggcagatca gccaggcctc ggccttggcc 60
196 ccggccccc cccaaatccct gccccaggct ccagccctg cccctgtcc agccatggta 120
198 tcaatctgg cccaggcccc agccctgtc ccagtcttag ccccaaggccc tcctcaggct 180
200 gtggcccccac ctgcccccaa gcccacccag gctggggaaag gaacgctgtc agaggccctg 240
202 ctgcagctgc agttttagta tgaagacctg ggggccttgc ttggcaacag cacagaccca 300
204 gctgtttca cagacccatggc atccgtcgac aactcccgat ttcagcagat gctgaaccag 360
206 ggcataccgt tggccccca cacaactgag cccatgtca tggagttaccc tgaggctata 420
208 actcgccctag tgacagccca gaggcccccc gacccagctc ctgtccact gggggccccc 480
210 gggctccca atggcccttct ttcaaggat gaagacttct cttccattgc ggacatggac 540
212 ttctcagccc tgctgagtc gatcagctcc taa 573
215 <210> SEQ ID NO: 12
216 <211> LENGTH: 36
217 <212> TYPE: DNA
218 <213> ORGANISM: Artificial Sequence
220 <220> FEATURE:

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221 <221> NAME/KEY: misc_feature
222 <222> LOCATION: (1)..(36)
223 <223> OTHER INFORMATION: primer
226 <400> SEQUENCE: 12
227 gcatgtctag agagatgtgg catgaaggcc tggaaag 36
230 <210> SEQ ID NO: 13
231 <211> LENGTH: 35
232 <212> TYPE: DNA
233 <213> ORGANISM: Artificial Sequence
235 <220> FEATURE:
236 <221> NAME/KEY: misc_feature
237 <222> LOCATION: (1)..(35)
238 <223> OTHER INFORMATION: primer
241 <400> SEQUENCE: 13
242 gcatcaactag tctttgagat tcgtcggaac acatg 35
245 <210> SEQ ID NO: 14
246 <211> LENGTH: 33
247 <212> TYPE: DNA
248 <213> ORGANISM: Artificial Sequence
250 <220> FEATURE:
251 <221> NAME/KEY: misc_feature
252 <222> LOCATION: (1)..(33)
253 <223> OTHER INFORMATION: primer
256 <400> SEQUENCE: 14
257 gcacattcta gaattgatac gcccagaccc ttg 33
260 <210> SEQ ID NO: 15
261 <211> LENGTH: 33
262 <212> TYPE: DNA
263 <213> ORGANISM: Artificial Sequence
265 <220> FEATURE:
266 <221> NAME/KEY: misc_feature
267 <222> LOCATION: (1)..(33)
268 <223> OTHER INFORMATION: primer
271 <400> SEQUENCE: 15
272 cgatcaacta gtaagtgtca atttccgggg cct 33
275 <210> SEQ ID NO: 16
276 <211> LENGTH: 36
277 <212> TYPE: DNA
278 <213> ORGANISM: Artificial Sequence
280 <220> FEATURE:
281 <221> NAME/KEY: misc_feature
282 <222> LOCATION: (1)..(36)
283 <223> OTHER INFORMATION: primer
286 <400> SEQUENCE: 16
287 gcactatcta gactgaagaa catgtgtgag cacagc 36
290 <210> SEQ ID NO: 17
291 <211> LENGTH: 36
292 <212> TYPE: DNA
293 <213> ORGANISM: Artificial Sequence

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Input Set : A:\346BUSC1.txt
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295 <220> FEATURE:
296 <221> NAME/KEY: misc_feature
297 <222> LOCATION: (1)..(36)
298 <223> OTHER INFORMATION: primer
301 <400> SEQUENCE: 17
302 gcactatcta gagtgagcga ggagctgatc cgagtg 36
305 <210> SEQ ID NO: 18
306 <211> LENGTH: 36
307 <212> TYPE: DNA
308 <213> ORGANISM: Artificial Sequence
310 <220> FEATURE:
311 <221> NAME/KEY: misc_feature
312 <222> LOCATION: (1)..(36)
313 <223> OTHER INFORMATION: primer
316 <400> SEQUENCE: 18
317 cgatcaacta gtggaaacat attgcagctc taagga 36
320 <210> SEQ ID NO: 19
321 <211> LENGTH: 36
322 <212> TYPE: DNA
323 <213> ORGANISM: Artificial Sequence
325 <220> FEATURE:
326 <221> NAME/KEY: misc_feature
327 <222> LOCATION: (1)..(36)
328 <223> OTHER INFORMATION: primer
331 <400> SEQUENCE: 19
332 cgatcaacta gttggcaacag ccaattcaag gtcccg 36
335 <210> SEQ ID NO: 20
336 <211> LENGTH: 31
337 <212> TYPE: DNA
338 <213> ORGANISM: Artificial Sequence
340 <220> FEATURE:
341 <221> NAME/KEY: misc_feature
342 <222> LOCATION: (1)..(31)
343 <223> OTHER INFORMATION: primer
346 <400> SEQUENCE: 20
347 atgctctaga ctgggggcct tgcttggcaa c 31
350 <210> SEQ ID NO: 21
351 <211> LENGTH: 31
352 <212> TYPE: DNA
353 <213> ORGANISM: Artificial Sequence
355 <220> FEATURE:
356 <221> NAME/KEY: misc_feature
357 <222> LOCATION: (1)..(31)
358 <223> OTHER INFORMATION: primer
361 <400> SEQUENCE: 21
362 atgctctaga gatgagttc ccaccatggt g 31
365 <210> SEQ ID NO: 22
366 <211> LENGTH: 39
367 <212> TYPE: DNA

RAW SEQUENCE LISTING ERROR SUMMARY
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Please Note:

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

Seq#:3; N Pos. 7,11

VERIFICATION SUMMARY**PATENT APPLICATION: US/10/002,244A****DATE: 04/18/2002****TIME: 14:12:55****Input Set : A:\346BUSC1.txt****Output Set: N:\CRF3\04182002\J002244A.raw**

L:61 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:3 after pos.:0